

FIGURE 1

SEQ ID NO:25 PAPCVIIASNIFVVAAFQIEKRLAVGALTEQMGLLHVVNLAIIICFPAAVALLVESITP
SEQ ID NO:26 PLEMCCLSLIFPLAAFTVEKLVLOKYISEPVVIFLHIIITMTEVLYPVVTLRCDSAFL
SEQ ID NO:02 PLEMCWISLSIFPLAAFTVEKLVLOKYISEPVGIFLHIIITMTEVLYPVVTLRCDSAFL
SEQ ID NO:08 PLLMCCLSLPIFPLGAFAVEKLAFAFNNLVSDPATTCFHILFTTFFEIVYPVLVILKCDSAVL
SEQ ID NO:14 PLLMCCLSLPAFPLGAFAVEKLAFAFNNVITDAVATCLHIFLSTTEIVYPVLVILKCDSAVL
SEQ ID NO:16 PLEMCCLSLVFPFAAFIVEKLAQKCIPEPVVVLHIIITSTSLFYPVLVILRCDSAFV
SEQ ID NO:22 PLLMCCLTLPFIPLAALMTEKWAQRKLIRDHVSILLHIIITTVLIYPVVVILKCESAVL
181 240

SEQ ID NO:25 VGSVFALASYSIMFLKLYSYRDVNLWCRRQRRVKAQVSTGKKVSGAAQAVSYPDNLTY
SEQ ID NO:26 SGVTLMLLT-CIVWLKLVSYAHTS--YDIRSL----ANAADKANP-----EVSYYVSL
SEQ ID NO:02 SGVTLMLLT-CIVWLKLVSYAHTS--YDIRSL----ANAADKANP-----EVSYYVSL
SEQ ID NO:08 SGFVLMFIA-CIVWLKLVSAHTN--HDIGKL----ITSGKKVDNELTAAGIDNLQXPTL
SEQ ID NO:14 SGFLLIFIA-CIVWLKLVSAHTN--HDIRQL----TMGGKKVDNELSTVMDMDNLQPPTL
SEQ ID NO:16 SGVTLMFLS-CVVWLKLVSYAHTN--YDMRAL----TKLVEKGEALLDTLNMDYPYNVSF
SEQ ID NO:22 SGFVLMFIA-SITWLKLVSAHTN--YDIRIL----SQSIEKGATHGSSIDEENIKGPTI
241 300

SEQ ID NO:25 RDLYYFIFAPTLCYELN-FPRSPRIRKRELLRRVLEMLFFTQLQVGLIQQWMVPTIQNSM
SEQ ID NO:26 KSLAYFMVAPTLCYQPS-YPRSACIRKGVARQFAKLVI FTGFMGFIIIEQYINPIVRNSK
SEQ ID NO:02 KSLAYFMVAPTLCYQPS-YPRSACIRKGVARQFAKLVI FTGFMGFIIIEQYINPIVRNSK
SEQ ID NO:08 GSLTYFKMAPTLCYQAKVILRTPYVRKGLVVRQVILYLI FTGLQGFIIIEQYINPIVNSQ
SEQ ID NO:14 GNLIYFMMAPTLCYQPS-YPRTSVVRKGLWIRQIILYLI FTGLQGFIIIEQYINPIVNSQ
SEQ ID NO:16 KSLAYFLVAPTLCYQPS-YPRTPYIRKGLWFRQLVKLI FTGVMGFIIIDQYINPIVQNSQ
SEQ ID NO:22 NSVVYFMLAPTLCYQPS-YPRTA FIRKGLWVTRQLIKCVVFTGLMGFIIIEQYINPIVQNSK
301 360

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ID NO:25	SEQ	KPFKMDYSRIIERLLKLAVPNHLIWLIIFFYWFHSCLNVAEELLQFGDREFYRDWNNAE																	
ID NO:26	SEQ	HPLKG-DLLYAIERVLKSPNLYVWLCMFYCFFHLWLNLIAELLCFGDREFYKDWWNAK																	
ID NO:02	SEQ	HPLKG-DLLYAIERVLKSPNLYVWLCMFYCFFHLWLNLIAELLCFGDREFYKDWWNAK																	
ID NO:08	SEQ	HPLMG-GLLNAVETVLKLSLPNVYLWLCMFYCLFHLWLNLIAELRFGDREFYKDWWNAK																	
ID NO:14	SEQ	HPLKG-GLLNAVETVLKLSLPNVYLWLCMFYAFFHLWLSILAEILRFGDREFYKDWWNAK																	
ID NO:16	SEQ	HPLKG-NLLYATERVLKLSVPNLYVWLCMFYCFFHLWLNLIAELLRFGDREFYKDWWNAK																	
ID NO:22	SEQ	HPLNG-NFLDAIERVLKSVPTLYVWLCMFYSEFFHLWLNLIAELLRFGDREFYKDWWNAK																	

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SEQ ID NO: 25	SVTYFWQNNWNPVHKWCIRHFYKPMRLRHGSSKWVARTGVLTSAFFHEYLVSVPLRMFRL
SEQ ID NO: 26	SVGDYWRMWNMPVHKWWMVRHIYFPCLRSKIPKTLAIIAFLVSAVFHELCLIAVPCRLFKL
SEQ ID NO: 02	SVGDYWRMWNMPVHKWWMVRHIYFPCLRSKIPKTLAIIAFLVSAVFHELCLIAVPCRLFKL
SEQ ID NO: 08	TIDYWRKWNMPVHKWIVRHIYFPCMRNGISKEVAVFISFFVSAVLHEYVLLFL-HILKF
SEQ ID NO: 14	TIDYWRKWNMPVHKWWMVRHIYFPCMRNGISKEVAVLISFLSVAVLHEICVAVPCRLKF
SEQ ID NO: 16	TVEDYWRMWNMPVHKWWMIRHLYFPCLRHGLPKAAALLAFLVSALFHELCLIAVPCHIFKL
SEQ ID NO: 22	TVEEYWRMWNMPVHKWIVRHIYFPCLRNGLSKGCAILIAFLVSAVFHELCLIAVPCHIFKL

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[illegible]

SESEQ	ID NO:25	WAF TAMMAQVPLAWIVGRFFQNGYNAAV-----WVTL-IIGQPVAVLMYVHDYVVLNYDAPVGV
SESEQ	ID NO:26	WAF LGIMFQVPLV-FITNYLQERF-GSTVGNMIFWFIFCFIQPQMCVLLYYHD--LMNRKGSMS-
SESEQ	ID NO:02	WAF LGIMFQVPLV-FITNYLQERF-GSTVGNMIFWFIFCFIQPQMCVLLYYHD--LMNRKGSMS-
SESEQ	ID NO:08	WAF LGIMLQIPLI-ILTSYLKNKFSDTMVGNMIFWFFFCIYGQPMCVLLYYHD--VMNR-TEKAK
SESEQ	ID NO:14	WAF LGIMLQIPLI-VLTAYLKSFRD TMVGNMIFWFFFCIYGQPMCLLLYYHD--VMNR-IEKAR
SESEQ	ID NO:16	WAF GGIMFQVPLV-LITNYLQNKFRNSMVGNMIFWFIFSLGQPMCVLLYYHD--LMNRKGLD-
SESEQ	ID NO:22	WAF SGIMFQIPLL-FLT KYLQDKFKNTMVGNMIFWFFFSIVGQPMCVLLYYHD--VMNRQAQTNG

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545

FIGURE 1

SEQ ID NO:25	MG-----DRGA-----GSSRRRTGSRVS-----VQGGGPKVEEDEVRDAVS	
SEQ ID NO:26	MAILDSAGVTTVTENGGEFVDLDRLRKRKSRSDSSNGLLLSGDNNSPSDDVGAPADVR	
SEQ ID NO:02	MAILDSAGVTTVTENGGEFVDLDRLRKRKSRSDSSNGLLLSGDNNSPSDDVGAPADVR	
SEQ ID NO:08	-----	
SEQ ID NO:14	MVSGDGDG-----DGGGGEAHAGGPRRRAGQ-----LRGLRDEAAGSPPRPRPR	
SEQ ID NO:16	MAISDEPESVATA-----LNHSSLRRRPSATSTAGLFNSPETTTDSSGDDDLAKDSGSD	
SEQ ID NO:22	MSKGNPDPHLP-----GSFLPSHGGPPPKPTPPRTFRNLPPSSSTHGPAAPSVAATAIAT	60
	1	
SEQ ID NO:25	PDLGAGGDAPAPAPAPAHTRDKDGRTSVGDG-----YW---DLRCHRLQD	
SEQ ID NO:26	DRIDSVVNDDAQGTANLAGDNNGGDNNGGGEGGEGRGNADATFTYRPSV-PAHRRARE	
SEQ ID NO:02	DRIDSVVNDDAQGTANLAGDNNGGDNNGGGEGGEGRGNADATFTYRPSV-PAHRRARE	
SEQ ID NO:08	-----	
SEQ ID NO:14	PRPRG---GDSNGRSVLRPGG-----GGGRGGGGDFS---AFTFRAA-APVHRKAKE	
SEQ ID NO:16	DSINS---DDAAVNSQQQNEK-----QDTDFSVLKFAFYRPSV-PAHRKVKE	
SEQ ID NO:22	TP-----PSASAAPLPPTVHGEAAH---GAAAAARRD-----ALLPGVGAHRRVKE	120
	61	
SEQ ID NO:25	SLFSSDSGFSNYR-GILNWCVVMLILSNARLFLENLIKYGILVDP-IQVVSFLKDPYSW	
SEQ ID NO:26	SPLSSDAIFKQSHAGLFNLCVVVLLIAVNSRLIIENLMKYGWLIRTDWFESSRSLRD---W	
SEQ ID NO:02	SPLSSDAIFKQSHAGLFNLCVVVLLIAVNSRLIIENLMKYGWLIRTDWFESSRSLRD---W	
SEQ ID NO:08	-----F--NATSLRD---W	
SEQ ID NO:14	SPLSSDAIFKQSHAGLFNLCIVVLVAVNSRLIIENLMKYGLLIRAGFWFNDKSLRD---W	
SEQ ID NO:16	SPLSSDTIFRQSHAGLFNLCIVVLVAVNSRLIIENLMKYGWLKSGFWFSSKSLRD---W	
SEQ ID NO:22	SPLSSDAIFRQSHAGLLNLCIVVLVAVNSRLIIENLMKYGLLIRAGFWFSARSLGD---W	180
	121	